Agenda

9:00 AM - 9:30 AM: Introduction to NSG
9:30 AM - 10:30 AM: Hands on Demo - How to use NSG

Speakers: Amit Majumdar, Subha Sivagnanam, Kenneth Yoshimoto, San Diego Supercomputer Center, University of California San Diego, La Jolla, USA
Ted Carnevale, Yale School of Medicine, New Haven, USA
Abstract of talk: We will introduce the Neuroscience Gateway (NSG) and mention what capabilities it provides, what neuronal simulations tools it provides for running free of charge on US NSF fund ed supercomputers. We will show how users can easily upload models, choose some parameters (e.g. number of cores , runtime etc.), run a simulation on parallel machines, and download results.

10:30 AM - 11:00 AM: Brian 2: spiking neural network simulation in Python with code generation

Speaker: Marcel Stimberg, Ãole Normale Supérieure and Institut de la Vision, Paris, France
Abstract of talk: Brian 2 is a fundamental rewrite of the Brian simulator for spiking neural networks. It is written in the Python programming language and focuses on simplicity and extensibility: neuronal and synaptic models, as well as connection patterns and synaptic delays can be described using mathematical notation. Based on these descriptions, code can be generated for different target languages and platforms, allowing the use on a variety of hardware.

11:00 AM - 11:30 AM: Modeling of cortical neurons in aging monkeys

Speaker: Timothy Rumbell, Mount Sinai School of Medicine, New York, USA
Abstract of talk: This project is led by Dr Patrick R Hof (Mount Sinai Schoo l of Medicine, New York, NY) and Dr Christina M Weaver (Franklin & Marshall College, Lancaster, PA). The project aims to investigate the cellular mechanisms underlying cognitive decline with aging in rhesus monkeys, the laboratory species most closely r elated to humans. Modeling is a significant portion of this project, which aims to pr edict cellular mechanisms that account for increased firing rates in layer 3 neocortical pyramidal neurons of aged versus young monkeys recorded in vitro. The construction of each model cell requires several stages. The electrophysiology of the neuron is characterized during in vitro experiments, while the neuron is filled with an intracellular dye. Next a 3D digital reconstruction of the cell.s morphology is obtained fro m high-resolution confocal

microscopy images, and imported into the NEURON simulation environment. Finally, models of several voltage- and calcium-gated ion channels are incorporated in order to simulate electrophysiological features recorded experimentally. This group plans to identify parameters for a total of ten model cells among three groups of rhesus monkeys: Young; Aged-Unimpaired (with cognitive testing scores matched to young monkeys); and Aged Impaired (with cognitive scores significantly impaired relative to young monkeys). Model parameters are tuned through an evolutionary algorithm which begins with an initial population of individuals each representing a distinct, randomly generated location in parameter space. Each individual is assigned a fitness value according to how accurately the model output reproduces empirical data. Fitter individuals have a high er probability of being maintained in a population. Crucial, largely open questions include (1) which channels are necessary to capture the observed behavior, (2) which parameters describing these channels must be optimized, (3) which electrophysiological features to include in the fitness function, and (4) what population size of the evolutionary algorithm is most appropriate.

11:30 AM - 12:00 PM:Using the NSG with a large-scale parallel computer model of the CA1 network: a case study

Speaker: Marianne Bezaire, University of California Irvine, Irvine, USA
Abstract of talk: My work focuses on compiling and implementing biological constraints into a large, realistic model of the rat hippocampal CA1 network. I use this network model to study physiological network oscillations in the CA1. As not all of the necessary biologically parameters of the network are known, I also have to explore the parameter space of my model to determine the robustness of my findings. This requires me to do a lot of data management, both of the biological constraints used in the model and of the simulations that I run to explore the parameter space. Here, I will show some techniques that I use to keep track of my data, code, and results, and how I use the NSG in my work.